

## REMARKS

Any fees that may be due in connection with the filing of this paper, or during the entire pendency of this application, may be charged to Deposit Account No. 02-1818. If a Petition for Extension of time is needed, this paper is to be considered such Petition.

Claims 1, 5-8, 21-23, 40, 46, 279, 307, 341, 343, 345 and 347-356 are pending in the application. Claims 1, 5-8, 21, 23, 46, 279, 307, 341, 345 and 347 are amended, claims 9, 16-19, 43, 44, 47-74, 139-144, 306, 308, 315, 316, 332-340, 342, 344, 346 are cancelled without prejudice, and claims 348-356 are added to focus prosecution on modified interferon alpha molecules that contain a mutation at E41Q in order to advance such claims to allowance. Also, in reviewing the claims, a few inadvertent typographical errors were found in claims 6 and 8. In order to advance prosecution, these are corrected herein.

### Response to Office Communication Concerning Non-Compliant Amendment

In the Amendment, mailed June 26, 2008, Applicant inadvertently provided a listing of the claims that did not include a listing for cancelled claim 342 and included the improper status identifier "Previously Presented" instead of the correct identifier "Currently Amended" for claim 345. Responsive to the Notice of Non-Compliant Amendment, mailed August 11, 2008, a complete listing of all claims, with proper status identifiers, is provided herein. No new matter is added.

### Sequence Listing

A review of the image file wrapper of the instant application in the Patent Application Information Retrieval (PAIR) website indicated an error in the sequence listing provided in the Amendment mailed June 26, 2008. In order to advance prosecution, a replacement sequence listing is provided herewith.

In the Amendment mailed June 26, 2008, Applicant provided an annotated substitute sheet to point out the amendment to SEQ ID NO:232 to insert the amino acid Phe (F) at position 38. Due to an inadvertent typographical error, the annotated substitute sheet provided in the amendment mailed June 26, 2008 incorrectly underlined the Phe (F) at position 43 instead of the inserted Phe (F) at position 38. Provided herein is a corrected annotated substitute sheet to indicate that SEQ ID NO:232 was amended to insert the amino acid Phe (F) at position 38.

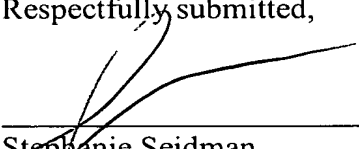
SEQ ID NO: 231 and its numeric identifiers are amended in order to comply with Sequence Listing disclosure rules set forth in 37 C.F.R §§1.821-1.823. The spacing within the sequence listing has also been corrected to separate the sequence into groups of 10 bases. The "n" at position 1 and the "n" at position 24 of the nucleotide sequence presented in SEQ ID NO: 231 have been replaced with "c" and "t" respectively. The <223> identifier of SEQ ID NO: 231 is replaced with three <223> identifiers to separately indicate the name of the sequence ("EMCV Probe") and refer to the RT-PCR probe label chemical groups as "FAM attached to 5' end of sequence" and "TAMR A attached to 3' end of sequence", respectively. References to "n" in the <223> identifier are removed. Therefore, the <221> and <222> numeric identifiers are deleted. Basis for these amendments can be found, for example, in the original sequence listing and in the specification as originally filed at page 133, lines 15-16, where SEQ ID NO: 231 is provided with "(FAM)" at the 5' end of the nucleotide sequence and "TAMR A" at the 3' end of the nucleotide sequence.

No new matter has been added.

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In view of the above, entry of this amendment and examination of the application are respectfully requested.

Respectfully submitted,



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**Applicant(s):** Rene Gantier et al.

**Title: RATIONAL EVOLUTION OF CYTOKINES FOR HIGHER STABILITY, THE CYTOKINES AND ENCODING NUCLEIC ACID MOLECULES**

<211> 166

<213> Art

**<223>**

Cys Asp L

Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
20 25 30

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
50 55 60

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
85 90 95

Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr  
115 120 125

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
145 150 155 160